

AMENDMENTS TO THE CLAIMS

Please amend the claims as follows:

1-103. (Cancelled)

104. **(Currently Amended)** A method for determining cancer prognosis or prediction for a human subject ~~monitoring gene expression~~ comprising:

(a) hybridizing a polynucleotide complementary to an intronic RNA sequence of a target gene to intronic RNA from a tissue sample that has been obtained from a human subject with cancer or a nucleic acid produced therefrom, to form a complex;

(b) quantitating the complex to determine the expression level of the target gene;

(c) normalizing the expression level of the target gene relative to the expression level of one or more reference genes in the tissue sample to determine a normalized expression level of the target gene;

(d) comparing said normalized expression level of said target gene to data based on normalized expression of the target gene in cancer tissue samples obtained from patients of known clinical outcome; and

(e) determining cancer prognosis or prediction for the human subject based on results obtained from step (d).

105. **(Cancelled)**

106. **(Previously Presented)** The method of claim 104, wherein the tissue sample is a resected tumor specimen or a tumor biopsy.

107. **(Previously Presented)** The method of claim 106, wherein the tissue sample is formalin-fixed paraffin-embedded tissue.

108. (Previously Presented) The method of claim 106, wherein the tissue sample comprises breast cancer tissue.

109. **(Cancelled)**

110. **(Currently Amended)** A method for determining cancer prognosis or prediction for a human subject ~~monitoring gene expression~~ comprising:

(a) hybridizing a polynucleotide that is immobilized on a solid support and complementary to an intronic RNA sequence of a target gene to intronic RNA from a tissue sample that has been taken from a human subject or a nucleic acid produced therefrom, to form a complex;

(b) quantitating the complex to determine the expression level of the target gene wherein the complex is quantitatively detected using an array;

(c) normalizing the expression level of the target gene relative to the expression level of one or more reference genes in the tissue sample to determine a normalized expression level of the target gene;

(d) comparing the normalized expression level of the target gene to data based on the normalized expression of the target gene in cancer tissue samples obtained from patients of known clinical outcome; and

(e) determining cancer prognosis or prediction for the human subject based on results obtained from step (d).

111. (Previously Presented) The method of claim 104, wherein the polynucleotide is a primer and the complex is quantitatively detected using quantitative PCR.

112. (Previously Presented) The method of claim 104, wherein the target gene is a human gene.

113. (Previously Presented) The method of claim 104, wherein the polynucleotide is an oligonucleotide.